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# Heritability Estimates for Fatty Acid Concentration in Angus Beef

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## Heritability Estimates for Fatty Acid Concentration in Angus Beef

### A. S. Leaflet R2191

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### Summary and Implications

Genetic control of fatty acid composition in grain-fed beef calves was evaluated when the fatty acids are measured on a percentage of lipid basis and on a mg of fatty acid / g of beef basis. Fatty acids of concern for human health (e.g. 14:0, 16:0, 16:1, 18:0, and 18:1) show evidence of having genetic control. Heritability estimates for these five fatty acids indicate stronger genetic control when fatty acid concentrations are expressed on a percentage of lipid basis ( $h^2 = 0.20$  to  $0.49$ ) than when expressed on a mg of fatty acid / g of beef basis ( $h^2 = 0.12$  to  $0.27$ ). However, there may be some concern that selection for a healthier fatty acid composition may come through an overall decrease of lipid within the beef. This would have significant consequences for production of high quality beef in the U.S. Our goal was to identify tools which will allow for selection of a healthier fatty acid profile with similar or increased lipid within beef. The results of this study indicate that a selection scheme based on fatty acids expressed on a percentage of lipid basis with maintenance of lipid concentration as a selection goal would be the most likely selection scheme to utilize for improving the healthfulness of U.S. beef.

### Introduction

Beef demand is influenced by the perceived healthfulness of the product. Beef generally has been classified as high in saturated fatty acids and this has driven some consumers away. Our group has reported previously that the percentage of fatty acids within the lipid does show evidence of being under genetic control. The objective of this study was to compare the heritability of fatty acids when expressed as a percentage of lipid to the heritability of fatty acids when expressed as a concentration within beef.

One of our concerns was that quantities of unsaturated and saturated fatty acids may be influenced by the overall percentage of lipid present in the sample because of relative quantities of phospholipid fatty acids vs. triacylglyceride fatty acids. It would be expected that the healthier fatty acid profiles would be present in the samples with low levels of intramuscular fat, as phospholipid fatty acids tend to have longer chained and more unsaturated fatty acids.

### Materials and Methods

Cattle from the Iowa State University beef breeding project and the Iowa Beef Center's Beef Tenderness project were used for this study. Cattle in this study were born in 2000, 2001, 2002, and 2003. A sample of the *Longissimus dorsi* without external connective tissue was collected from 915 Angus-sired bulls and steers managed under a grain-fed calf feeding system. These samples were evaluated for fatty acid composition by gas chromatography. Some fatty acids were not able to be individually separated with gas chromatography and were measured as a combination of two fatty acids {e.g. 20:3(n3) + 20:4(n6); 22:2(n6) + 20:5(n3)}.

First, fatty acid concentrations were expressed as g of fatty acid / 100 g of lipid (lipid basis). Percentage lipid within the beef sample then was used to calculate fatty acid concentrations as mg of fatty acid / g of beef (beef basis). Within each measurement system for fatty acids several ratios of fatty acids were calculated to represent function and variation in biochemical pathways.

In particular, the Atherogenic Index (AI), a measure of healthfulness of lipid composition, was calculated as:

$$AI = \frac{(4 * 14 : 0) + 16 : 0}{\sum(MUFAs) + \sum(PUFAs)} \text{ (lipid based only),}$$

where MUFAs are monounsaturated fatty acids and PUFAs are polyunsaturated fatty acids.

Three fatty acid desaturase ratios were calculated.

The ratio of 16:1 to 16:0 (16:1/16:0) was calculated as:

$$(16 : 1 / 16 : 0) = \frac{16 : 1}{16 : 0}$$

The ratio of 18:1 to 18:0 (18:1/18:0) was calculated as:

$$(18 : 1 / 18 : 0) = \frac{18 : 1}{18 : 0}$$

The combination desaturase ratio of X:1 to X:0 (X:1/X:0)

$$\text{was calculated as: } (X : 1 / X : 0) = \frac{16 : 1 + 18 : 1}{16 : 0 + 18 : 0}$$

Two fatty acid chain elongation ratios were calculated.

The ratio of 16:0 to 14:0 (16/14) was calculated as:

$$(16 / 14) = \frac{16 : 0}{14 : 0}$$

The ratio of 18:0 to 16:0 (18/16) was calculated as:

$$(18 / 16) = \frac{18 : 0}{16 : 0}$$

Heritability of each of the fatty acids was estimated using the sire model option of MTDFREML. Management contemporary group was the only fixed effect included in

the model. For this study, management contemporary group was defined from herd of origin, gender, feedlot dietary treatment, and harvest date. Heritability estimates are reported from the first convergence of the model, where the variance of the simplex was less than  $10^{-10}$ . Samples came from 87 sires with one to 41 progeny.

### Results and Discussion

Means and standard deviations for the various fatty acids when expressed on the percentage of lipid basis as well as the mass within beef basis are reported in Table 1. Average percentage lipid in these beef samples was 4.55 % with a standard deviation of 1.77 %. Fatty acids with the largest quantities in these samples were 16:0, 18:0, and 18:1.

Heritability estimates and standard error of the heritability estimate for fatty acid concentrations expressed under both the lipid and beef method are presented in Table 2. Percentage lipid heritability was 0.14 with a standard error of the estimate of 0.084 in this data set. Fatty acids of interest for human health and showing the largest heritability estimates in beef were 14:0, 16:0, 16:1, 18:0, and 18:1. These five fatty acids all show heritability estimates of 0.20 to 0.49 when expressed on a percentage of lipid basis, which indicates that they should respond to selection pressure. When expressed on the mass within beef basis the heritability estimates are lower, but these same five fatty acids still show the largest genetic control with heritabilities of 0.12 to 0.27. Part of this decrease in fatty acid heritability when expressed on the beef basis is likely due to the use of percentage lipid to calculate the mass of fatty acids present in beef, because percentage lipid only had a heritability of 0.14.

The fatty acid concentrations of 14:0, 16:0, 16:1, 18:0, and 18:1 all showed stronger phenotypic correlations to lipid percentage when the fatty acids were expressed on the mg of fatty acid per g of beef basis ( $r = 0.906$  to  $r = 0.989$ ) than when expressed on the g of fatty acid per 100 g of lipid basis ( $r = 0.069$  to  $r = 0.533$ ). Therefore, expression of fatty acids on the beef basis is driven to a greater extent by the variation in concentration of lipid than by the variation in proportion of specific fatty acid within the lipid. As shown in Table 3, concentrations of 14:0 in beef are changed much more by changes in the percentage of lipid (0.83 to 1.17 mg 14:0 / g of beef) than changes in percentage of 14:0 within the lipid (0.28 to 0.62 mg 14:0 / g of beef). This indicates that selection for more healthful fatty acid profiles will be

detrimental to the concentration of lipid within beef if selection was based on the mgs of fatty acid per g of beef.

While the AI shows a considerable amount of genetic control ( $h^2 = 0.52$ ), selection would need to be made for targeted increase of desirable and decrease of undesirable fatty acids. Because AI is a ratio, there could be different values of desirable and undesirable fatty acids that give a similar AI ratio. If selection were placed on the AI ratio, selection may not result in a directed change of fatty acids. A more effective approach would be to develop a selection index to appropriately weight the desired changes in fatty acids to use for selection.

Desaturase and elongation activity both show evidence of genetic control with heritability estimates of 0.24 to 0.41 under both methods of expressing the levels of fatty acid concentration. These results also provide optimism for being able to make genetic selection for more healthful beef. Further studies that need to be investigated include genetic correlations between the various fatty acid concentrations and lipid percentage to better enable multiple trait selection for increasing healthfulness of the lipid while maintaining or increasing lipid concentrations.

### Implications

Beef fatty acids of concern for human health show evidence of having genetic control. On the basis of heritability estimates, this genetic control is larger when the fatty acid concentrations are expressed on a percentage of lipid basis. Because fatty acid concentration expressed as a proportion of beef is more closely related to concentration of lipid and it shows typically lower heritability values it would be the less desirable method to use for selection. These results indicate that a selection scheme based on fatty acids expressed on a percentage of lipid basis with maintenance of lipid concentration as a selection goal would be the most likely selection scheme to utilize for improving the healthfulness of U.S. beef.

### Acknowledgements

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**Table 1. Means and standard deviations for several fatty acids when expressed on a percentage of lipid or a mass within beef basis.**

Fatty Acid	Mean, Lipid (g of fatty acid / 100 g of lipid)	S. D. <sup>a</sup> , Lipid	Mean, Beef (mg of fatty acid / g of beef)	S. D. <sup>a</sup> , Beef
14:0	2.81	0.49	1.24	0.60
14:1(n5)	0.68	0.28	0.31	0.19
15:0	0.36	0.17	0.15	0.10
16:0	26.48	1.94	11.26	4.85
16:1(n7)	3.48	0.67	1.51	0.71
17:0	1.00	0.26	0.44	0.23
18:0	12.74	1.44	5.38	2.33
18:1(n7,n9)	41.34	3.26	17.83	7.98
18:2(n6)	7.02	2.99	2.25	0.76
18:3(n6)	0.05	0.07	0.02	0.03
20:0	0.02	0.04	0.01	0.02
18:3(n3)	0.20	0.09	0.07	0.04
20:1(n9)	0.09	0.11	0.04	0.06
20:2(n6)	0.07	0.06	0.03	0.03
20:3(n6)	0.45	0.21	0.13	0.05
22:0	0.02	0.06	0.01	0.02
20:3(n3)+20:4(n6)	2.03	0.98	0.58	0.16
22:1(n6)	0.01	0.02	0.00	0.01
22:2(n6)+20:5(n3)	0.18	0.17	0.05	0.03
24:0	0.02	0.05	0.01	0.02
22:4(n6)	0.28	0.15	0.08	0.03
24:1	0.05	0.05	0.02	0.02
22:5(n3)	0.50	0.25	0.14	0.05
22:6(n3)	0.10	0.15	0.03	0.06
AI <sup>b</sup>	0.67	0.08	N.A. <sup>c</sup>	N.A. <sup>c</sup>
<b>Desaturase Ratios, no unit label</b>				
16:1/16:0 <sup>d</sup>	0.13	0.02	0.13	0.02
18:1/18:0 <sup>e</sup>	3.29	0.50	3.32	0.50
X:1/X:0 <sup>f</sup>	1.15	0.11	1.16	0.11
<b>Elongation Ratios, no unit label</b>				
16/14 <sup>g</sup>	9.64	1.55	9.43	1.45
18/16 <sup>h</sup>	0.49	0.08	0.48	0.08

<sup>a</sup> S. D. = standard deviation.

<sup>b</sup> AI = atherogenic index

<sup>c</sup> N.A. = not applicable when the fatty acids are not expressed as a percentage of the lipid.

<sup>d</sup> 16:1/16:0 = concentration 16:1 / concentration 16:0

<sup>e</sup> 18:1/18:0 = concentration 18:1 / concentration 18:0

<sup>f</sup> X:1/X:0 = concentration (16:1+18:1) / concentration (16:0+18:0)

<sup>g</sup> 16/14 = concentration 16:0 / concentration 14:0

<sup>h</sup> 18/16 = concentration 18:0 / concentration 16:0

**Table 2. Heritability estimate and standard error of heritability estimate for several fatty acids when expressed on a percentage of lipid or a mass within beef basis.**

	$h^2$ , Lipid	$h^2$ s.e. <sup>a</sup> , Lipid	$h^2$ , Beef	$h^2$ s.e. <sup>a</sup> , Beef
14:0	0.49	0.140	0.19	0.092
14:1(n5)	0.13	0.080	0.11	0.076
15:0	0.10	0.076	0.10	0.068
16:0	0.43	0.132	0.17	0.088
16:1(n7)	0.49	0.140	0.27	0.108
17:0	0.13	0.080	0.17	0.088
18:0	0.20	0.092	0.12	0.076
18:1(n7,n9)	0.38	0.132	0.16	0.088
18:2(n6)	0.23	0.100	0.06	0.068
18:3(n6)	0.03	0.056	0.00	0.056
20:0	0.02	0.052	0.03	0.060
18:3(n3)	0.08	0.068	0.04	0.056
20:1(n9)	0.00	0.068	0.00	0.056
20:2(n6)	0.00	0.060	0.00	0.056
20:3(n6)	0.22	0.096	0.13	0.076
22:0	0.00	0.044	0.00	0.044
20:3(n3)+20:4(n6)	0.26	0.104	0.12	0.076
22:1(n6)	0.00	0.044	0.00	0.048
22:2(n6)+20:5(n3)	0.07	0.068	0.04	0.056
24:0	0.00	0.052	0.00	0.040
22:4(n6)	0.19	0.088	0.10	0.068
24:1	0.01	0.044	0.00	0.040
22:5(n3)	0.16	0.088	0.06	0.068
22:6(n3)	0.00	0.040	0.00	0.052
AI <sup>b</sup>	0.52	0.144	N.A. <sup>c</sup>	N.A. <sup>c</sup>
<b>Desaturase ratios, no unit label</b>				
16:1/16:0 <sup>d</sup>	0.40	0.128	0.40	0.128
18:1/18:0 <sup>e</sup>	0.25	0.104	0.24	0.100
X:1/X:0 <sup>f</sup>	0.41	0.132	0.41	0.132
<b>Elongation ratios, no unit label</b>				
16/14 <sup>g</sup>	0.31	0.116	0.34	0.120
18/16 <sup>h</sup>	0.29	0.108	0.29	0.108

<sup>a</sup> s.e. = standard error of the heritability estimate.

<sup>b</sup> AI = atherogenic index.

<sup>c</sup> N.A. = not applicable when the fatty acids are not expressed as a percentage of the lipid.

<sup>d</sup> 16:1/16:0 = concentration 16:1 / concentration 16:0

<sup>e</sup> 18:1/18:0 = concentration 18:1 / concentration 18:0

<sup>f</sup> X:1/X:0 = concentration (16:1+18:1) / concentration (16:0+18:0)

<sup>g</sup> 16/14 = concentration 16:0 / concentration 14:0

<sup>h</sup> 18/16 = concentration 18:0 / concentration 16:0

**Table 3. Demonstration of variation in lipid percentage being more significant than variation in percent of particular fatty acid (14:0) in calculating concentrations of fatty acid on a mg of beef basis.**

	Lipid Percentage		Lipid percentage effect <sup>b</sup>
	Mean - 1 S.D. <sup>a</sup> (2.78 %)	Mean + 1 S.D. <sup>a</sup> (6.32 %)	
14:0 as percentage of lipid			
Mean - 1 S.D. (2.32 %)	0.64 <sup>c</sup>	1.47 <sup>c</sup>	<b>0.83<sup>c</sup></b>
Mean + 1 S.D. (3.30 %)	0.92 <sup>c</sup>	2.09 <sup>c</sup>	<b>1.17<sup>c</sup></b>
14:0 percentage effect <sup>d</sup>	<b>0.28<sup>c</sup></b>	<b>0.62<sup>c</sup></b>	

<sup>a</sup> S.D. = standard deviation

<sup>b</sup> difference from (Lipid percentage mean + 1 S.D.) – (Lipid percentage mean – 1 S.D.)

<sup>c</sup> mg 14:0 / g of beef

<sup>d</sup> difference from (14:0 percentage of lipid mean + 1 S.D.) – (14:0 percentage of lipid mean – 1 S.D.)